## REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated September 9, 2003. In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

Claims 3-13 are under consideration in this application. Claims 1-2 are being cancelled without prejudice or disclaimer. Claims 3-8 being amended, as set forth in the above marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention. Claims 9-13 are being added to recite other embodiment described in the specification.

Additional Amendments

The Abstract and the claims are being amended to correct formal errors and/or to better recite or describe the features of the present invention as claimed. All the amendments to the claims are supported by the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formality Rejection

The abstract was objected due to the abstract being over 150 words, and has requested corrections. Claims 1-8 were rejected under 35 U.S.C. § 112, second paragraph, on the grounds of being indefinite. As indicated, the abstract and the claims have been amended as required by the Examiner. Accordingly, the withdrawal of the outstanding informality rejection is in order, and is therefore respectfully solicited.

Prior Art Rejections

Claims 1-2 were rejected under 35 U.S.C. 102(b) as being anticipated by an article by Schena et al published on Proceedings of the National Academy of Sciences, Vol. 93, 1996,

pp.10614-10619 (hereinafter "Schena"). This rejection has been carefully considered, but is most respectfully traversed.

The method for displaying gene expression data of the invention (Fig. 2), as now recited in claim 3, comprises: calculating a first ratio (e.g., b/a) of expression levels of each of a plurality of genes in a first experiment between a Sample A and a Sample B; calculating a second ratio (e.g., c/A) of expression levels of said each of a plurality of genes in a second experiment between the Sample A and a Sample C; and displaying marks (e.g., (b/a, c/A, 1), ((R/r)(b/a), (R/r)(c/A), R/r)), ((K/r)(b/a), (K/r)(c/A), K/r)) ) of a first product of the first ratio and a constant, a second product of the second ratio and the constant, and the constant on coordinate positions with respect to x-, y- and z-axes on or inside a surface of a sphere. The constant (e.g., 1, R/r, or K/r) is determined to make the marks viewable ("*a constant value for adjusting the display to be viewable through enlargement or reduction*" page 16, lines 15-16). The definitions of a, b, A, c, r, R, K are described on pages 15-16 and recited in the new claims.

As recited in claims 5, 6, and 12, the method (Figs. 7-8) further comprises: performing a clustering analysis on the displayed marks (b/a, c/A, 1), the magnitude coordinate positions ((R/r)(b/a), (R/r)(c/A), R/r)), or the surface coordinate positions ((K/r)(b/a), (K/r)(c/A), K/r)) on or inside the sphere; and marking at least one gene group obtained by the clustering analysis as a region on the sphere.

As recited in claims 7-8 (Figs. 11, 13), the expression level data is data in a time series, and the data and the region of a gene group are displayed based on respective time points in conjunction with a direction of changes of the coordinate positions or the region with time in the displaying step.

As such, the present invention provides a visual display which is useful in roughly understanding the state of groupings and changes, by comparing expression data of genes from two experiments based on expression data of one sample common to both experiments. In order to compare data of expression levels obtained from different experiments, the expression levels are displayed in three-dimension as linked by the data of the common sample used in both experiments (Abstract).

Applicants respectfully contend that Schena fails to teach or suggest such as visual displaying method using "**two ratios** of expression levels of each of a plurality of between Samples A and B in a first experiment and between Samples A and C in a second experiment **as**

**coordinate positions with respect to x-, y- and z-axes on or inside a surface of a sphere**" so as to link and display the expression level data as does the invention.

In contrast, Schena merely "***takes the average*** *of the ratios of two independent hybridization* (page 10614, 2nd col. last two lines)," and Figs. 2-3 of Schena do not resemble Figs. 7-8, 11, 13 of the invention in any way.

As such, the present invention as now claimed is distinguishable and thereby allowable over the rejection raised in the Office Action. The withdrawal of the outstanding prior art rejections is in order, and is respectfully solicited.

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art reference upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

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## SUBSTITUTE ABSTRACT OF THE DISCLOSURE

The expression level data for Samples A and B in a first experiment and expression level data for Samples A and C in a second experiment are combined and converted into single three dimensional data and displayed as points inside a sphere for visual display. Alternatively, the ratios of the expression level data of the Samples A, B and C are mapped on or inside a sphere. A clustering analysis is performed based on the distributed points inside or on the sphere to visually display the expression states of genes for the three types of samples. In addition, the expression level data displayed as points inside or on the sphere are linked by a line or a curve for each gene or for each gene group resulting from the clustering analysis, to visually display the changes of expression states with time.